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Evaluating summarised radionuclide concentration ratio datasets for wildlife

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ABSTRACT

Concentration ratios ($CR_{wo\text{-}media}$) are used in most radioecological models to predict whole-body radionuclide activity concentrations in wildlife from those in environmental media. This simplistic approach amalgamates the various factors influencing transfer within a single generic value and, as a result, comparisons of model predictions with site-specific measurements can vary by orders of magnitude. To improve model predictions, the development of 'condition-specific' $CR_{wo\text{-}media}$ values has been proposed (e.g. for a specific habitat). However, the underlying datasets for most $CR_{wo\text{-}media}$ value databases, such as the wildlife transfer database (WTD) developed within the IAEA EMRAS II programme, include summarised data. This presents challenges for the calculation and subsequent statistical evaluation of condition-specific $CR_{wo\text{-}media}$ values. A further complication is the common use of arithmetic summary statistics to summarise data in source references, even though $CR_{wo\text{-}media}$ values generally tend towards a lognormal distribution and should, therefore, be summarised using geometric statistics. In this paper, we propose a statistically-defensible and robust method for reconstructing underlying datasets to calculate condition-specific $CR_{wo\text{-}media}$ values from summarised data and deriving geometric summary statistics. This method is applied to terrestrial datasets from the WTD. Statistically significant differences in sub-category $CR_{wo\text{-}media}$ values (e.g. mammals categorised by feeding strategy) were identified, which may justify the use of these $CR_{wo\text{-}media}$ values for specific assessment contexts. However, biases and limitations within the underlying datasets of the WTD explain some of these differences. Given the uncertainty in the summarised $CR_{wo\text{-}media}$ values, we suggest that the $CR_{wo\text{-}media}$ approach to estimating transfer is used with caution above screening-level assessments.

1. Introduction

Concentration ratios ($CR_{wo\text{-}media}$) are equilibrium transfer parameters which are used to predict wildlife transfer in most models that have been developed for assessing the impact of ionising radiation on wildlife under chronic exposure conditions (Beresford et al., 2008a). Also known as the Biological Concentration Factor (BCF), Concentration Factor (CF), Biological Intake Value (B_{iv}), Transfer Factor (TF) or Lumped Parameter, the $CR_{wo\text{-}media}$ is a coefficient which relates the whole-body ($_{wo}$) activity concentration of a radionuclide (R_{act}) in an organism on a fresh mass (fm) basis to the activity concentration of that radionuclide in an environmental medium ($_{media}$). Depending on the environment and radionuclide under consideration, the reference medium may be soil, sediment, water or air. If soil or sediment, the activity concentration in the environmental medium is reported as dry mass (dm).

For terrestrial ecosystems, Beresford et al. (2008b) defined the $CR_{wo\text{-}media}$ value as:

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$$CR_{wo-soil} = \frac{R_{act} \text{ in biota whole} - \text{body } (\text{Bq kg}^{-1} \text{ fm})}{R_{act} \text{ in soil } (\text{Bq kg}^{-1} \text{ dm})} \quad (1)$$

with the exception of chronic atmospheric releases of ^{3}H, ^{14}C, $^{32,33}P$ and ^{35}S, which are defined as:

$$CR_{wo-air} = \frac{R_{act} \text{ in biota whole} - \text{body} (\text{Bq kg}^{-1} \text{fm})}{R_{act} \text{ in air} (\text{Bq m}^{-3})} \quad (2)$$

For aquatic ecosystems, Hosseini et al. (2008) define the $CR_{wo-media}$ as:

$$CR_{wo-water} = \frac{R_{act} \text{ in biota whole} - \text{body} (\text{Bq kg}^{-1} \text{fm})}{R_{act} \text{ in filtered water} (\text{Bq l}^{-1})} \quad (3)$$

although some models use sediment as the medium for aquatic ecosystems (Copplestone et al., 2013).

Recent work within the International Atomic Energy Agency (IAEA) EMRAS II programme has led to the development of a Wildlife Transfer Database (WTD, http://www.wildlifetransferdatabase.org/), which provides the most comprehensive compilation of $CR_{wo-media}$ values available to date for both terrestrial and aquatic ecosystems (Copplestone et al., 2013). The $CR_{wo-media}$ values within the WTD have been calculated from direct measurements of wildlife whole-body activity concentrations and/or from tissue measurements converted to whole-body estimates using conversion factors (e.g. Wood et al., 2010; Yankovich et al., 2010) if the information is not given in the source paper. The WTD has collated both radioisotope and stable element data for a range of elements that may need to be considered within environmental radiation protection assessments. The WTD has been used to provide summarised $CR_{wo-media}$ statistics for an IAEA handbook (IAEA, 2013) and an International Commission on Radiological Protection report (ICRP, 2009). Although $CR_{wo-media}$ values are used widely within all tiers of environmental radiation protection assessments (from initial screening assessments to detailed assessments involving the use of $CR_{wo-media}$ value probability density functions), there have been various criticisms of the $CR_{wo-media}$ value approach.

A criticism of the $CR_{wo-media}$ approach is the simplistic assumption that all of the complexity associated with radionuclide behaviour within environmental media, the interaction of organisms with these media and subsequent food chain transfer can be appropriately represented by a simple ratio. For instance, the assumption of instantaneous equilibrium between organism and medium is unrealistic (e.g. Mann et al., 2007) and various factors will influence uptake. These factors include physico-chemical influences on uptake (Vives i Batlle, 2012), such as pH, cation exchange capacity, concentrations of chemical analogues and temperature (Jeffree, 1991; Whicker et al., 1990), heterogeneity of contaminant distribution (Beresford et al., 2005), the effect of seasonal changes in both the endocrine cycle and diet (Scott et al., 1986; Rudge et al., 1993; Wood et al., 2009a) and organism age (Albrecht et al., 2007; Gochfeld and Burger, 1987; Sakai et al., 2000), especially for radionuclides with a long biological half-life (ICRP, 2009). Non-linearity of transfer has also been reported for some elements/radionuclides, with different transfer values being calculated for different media concentrations (Tuovinen et al., 2011) although data from sites with high heavy metal concentrations, at which non-linear transfer may be observed, were excluded from the WTD (Copplestone et al., 2013).

As a result of the complex interactions of factors influencing transfer, comparisons between predicted and measured radionuclide activity concentrations in wildlife can vary by several orders of magnitude (e.g. Beresford et al., 2008c,d; Johansen et al., 2012; Wood et al., 2009b). Recognising this variability in comparisons between predictions and measurements of whole-body radionuclide activity concentrations and the underlying complexity of radionuclide transfer, the adoption of mechanistic modelling approaches for predicting transfer has been identified in the Strategic Research Agenda developed through the EC Strategy for Allied Radioecology (STAR) project (Hinton et al., 2013; http://www.star-radioecology.org) as a priority for radioecology research over the next 20 years.

Some of the criticisms of using $CR_{wo-media}$ values to predict transfer are, in part, countered by the lack of available data to parameterise mechanistic models (ICRP, 2009; Wood et al., 2009b) and the potential to calculate condition-specific $CR_{wo-media}$ values, such as for different broad soil types as done in human food chain modelling (e.g. IAEA, 2009). Improving the parameter database for mechanistic models is one of the objectives of the forthcoming International Atomic Energy Agency's MOdelling and DAta for Radiological Impact Assessments (MODARIA) programme (http://goto.iaea.org/modaria). However, the extent to which available data can be used to calculate condition-specific $CR_{wo-media}$ values, such as for ecosystem and organism sub-categories, needs further evaluation.

Recognising both the conflicting viewpoints surrounding the applicability of $CR_{wo-media}$ values and the significant international effort to develop the WTD, there is a need to critically review the equilibrium transfer parameter approach and to provide some clear guidance on the application of this approach within environmental radiation protection. In this paper, we propose a method for evaluating summarised CR datasets and assess the extent to which terrestrial ecosystem data within the WTD can be disaggregated to produce $CR_{wo-media}$ values for ecosystem and organism sub-categories (see Tables 1 and 2).

1.1. Summarising $CR_{wo-media}$ values in the WTD

The WTD provides summary tables of $CR_{wo-media}$ values for organism group and radionuclide combinations across generic ecosystems (terrestrial, freshwater, brackish and marine) (Howard et al., 2013a). Where the number of values across all studies in the whole dataset (N) for a given organism radionuclide combination is greater than 2 and the available $CR_{wo-media}$ values are all individual values, the summarised data are presented as the arithmetic mean (μ) and standard deviation (σ):

$$\mu = \frac{\sum_{i=1}^{N} x_i}{N} \quad (4)$$

$$\sigma = \sqrt{\frac{\sum_{i=1}^{N} (x_i - \mu)^2}{N-1}} \quad (5)$$

where x_i represents each value (x) from 1 to N and all other terms have been defined. The $CR_{wo-media}$ values are entered into the WTD as either individual values or summarised data: the number of observations in a study (n_i)[1], arithmetic mean and standard deviation for individual studies. Therefore weighted arithmetic mean (μ_w) and associated standard deviation (σ_w) are calculated using Equations (6) and (7) respectively (Howard et al., 2013a):

$$\mu_w = \frac{\sum_{i=1}^{n} n_i CR_i}{N} \quad (6)$$

[1] $N = \Sigma n_i$.

Table 1
Terrestrial organism groupings and sub-categories used for collating data within the Wildlife Transfer Database (Copplestone et al., 2013).

Broad group	Available sub-categories
Amphibian	–
Annelid	
Arachnid	–
Arthropod	Arthropod – Carnivorous
	Arthropod – Detritivorous
	Arthropod – Herbivorous
Bird	Bird – Carnivorous
	Bird – Herbivorous
	Bird – Omnivorous
Mollusc – gastropod	–
Grasses and herbs	–
	Grasses
	Herbs[a]
Lichens and Bryophytes	–
Mammal	Mammal – Carnivorous
	Mammal – Herbivorous[b]
	Mammal – Omnivorous
	Mammal – Marsupial[c]
	Mammal – *Rangifer* spp.
Reptile	–
	Reptile – Carnivorous
	Reptile – Herbivorous
Shrub	–
Tree	–
	Tree – Coniferous
	Tree – Broadleaf

[a] Any non-woody plant which does not fall into one of the other categories.
[b] Excludes *Rangifer* spp. (reindeer and caribou) in recognition of the high transfer of some elements to this group compared to other mammals.
[c] No distinction made between marsupials based on feeding strategy.

$$\sigma_w = \sqrt{\frac{\sum_{i=1}^{n}\left((n_i-1)\sigma_i^2 + n_i \mathrm{CR}_i^2\right) - \frac{\left(\sum_{i=1}^{n} n_i \mathrm{CR}_i\right)^2}{N}}{N-1}} \quad (7)$$

where CR_i is the arithmetic mean $CR_{wo\text{-}media}$ value used in the derivation of the summarised data for study i, n is the number of studies and all other terms have been defined. The range (minimum and maximum values) of the weighted dataset is also presented in the WTD. However, because the weighted dataset is derived from a combination of individual values (i.e. entries where $n_i = 1$) and summarised datasets, the minimum and/or maximum value may be the arithmetic mean of one of the input datasets rather than the overall range derived from all of the underlying data (Copplestone et al., 2013).

$CR_{wo\text{-}media}$ values tend to be lognormally distributed (Beresford et al., 2008a; Brown et al., 2008); transforming $CR_{wo\text{-}media}$ values by taking the natural logarithm (ln) of the individual data values within the distribution produces a dataset with the properties of a normal distribution. Therefore, although summarised $CR_{wo\text{-}media}$ data are generally presented using the arithmetic mean and standard deviation, from a statistical analysis perspective that approach is often incorrect because it implies that the untransformed data follow a normal distribution. The correct approach for describing the central tendency and variability of a lognormally distributed dataset (assuming all entries are individual values) is to calculate the geometric mean (μ_g) and its associated standard deviation (σ_g):

$$\mu_g = \sqrt[N]{x_i x_{i+1} \cdots x_N} \quad (8)$$

$$\sigma_g = \exp\left(\sqrt{\frac{\sum_{i=1}^{N}\left(\ln\frac{x_i}{\mu_g}\right)^2}{N}}\right) \quad (9)$$

However, because many of the data inputs into the WTD are of summarised data and the geometric mean and standard deviation are rarely presented in the source references, the above approach to deriving geometric means and standard deviations cannot be applied readily across the whole WTD. As some users may want geometric values, the WTD uses the weighted arithmetic mean and associated standard deviation to estimate weighted geometric means (μ_{gw}) and standard deviations (σ_{gw}) for the weighted dataset (IAEA, 2013):

$$\mu_{gw} = \exp\left(-0.5\ln\left(\frac{\sigma_w^2 + \mu_w^2}{\mu_w^4}\right)\right) \quad (10)$$

$$\sigma_{gw} = \exp\left(\sqrt{\ln\left(\frac{\sigma_w^2 + \mu_w^2}{\mu_w^2}\right)}\right) \quad (11)$$

There are a number of challenges in summarising data within the WTD:

(i) Although the WTD presents $CR_{wo\text{-}media}$ values for some organism sub-categories, the decision to present these data was based on the number of values available for each sub-category and the significance of any differences was not considered. Testing the significance of differences between sub-category $CR_{wo\text{-}media}$ values is not straightforward because the datasets used within the WTD include both individual and summarised data.
(ii) As noted previously, the range of $CR_{wo\text{-}media}$ values in the WTD summary tables may be the range of arithmetic means rather than of underlying data. Therefore, users of the WTD are unable to assess the 'true' range of the underlying data, which may be important for screening assessments if the maximum value is used (e.g. USDoE, 2002).
(iii) Some of the data entries within the WTD provide n_i and arithmetic mean $CR_{wo\text{-}media}$, but no standard deviation. These data entries were used n_i times within the derivation of arithmetic summary statistics in IAEA (2013).

Table 2
Terrestrial ecosystem sub-categories used within the Wildlife Transfer Database (Copplestone et al., 2013); definitions are from (IAEA, 2013).

Ecosystem sub-category	Definition
Terrestrial	Generic ecosystem including all terrestrial ecosystem types (excludes terrestrial areas of estuarine systems)
Terrestrial – semi-natural grassland	Includes: mountain and upland grasslands, heath and shrub lands, and some Arctic ecosystems
Terrestrial – forest	Land with tree crown cover of more than 10% over an area of more than 0.5 ha and with trees, which are able to reach a minimum *in situ* height of 5 m at maturity
Terrestrial – agricultural grassland	Managed grasslands
Terrestrial – coastal sand dunes	Coastal sand dunes (excludes marine organisms)
Terrestrial – wetland	Marsh, fen, peatland (excludes estuarine saltmarshes)

(iv) The estimation of the weighted geometric mean and standard deviation from the weighted arithmetic mean and standard deviation may result in poor estimates of the geometric parameters, especially when the underlying arithmetic data include summarised data where $n_i > 2$ but no standard deviation (σ_i) is reported. As can be seen in Equations (10) and (11), the calculation of geometric summary statistics utilises the arithmetic standard deviation and this is likely to be underestimated where datasets include entries with $n_i > 2$ but no standard deviation.

To analyse the statistical significance of differences in $CR_{wo\text{-}media}$ values within specific organism and/or ecosystem sub-categories, it is necessary to identify a method that enables such analyses to be performed on weighted datasets, taking into account that the WTD includes summarised data entries with missing arithmetic standard deviation values. The ideal approach would be to access the underlying data for each individual study for which summarised data have been entered into the WTD. However, with more than 520 data sources from the period 1956 to 2010 providing data to the WTD, this approach is impossible. In the subsequent sections we propose and discuss a database reconstruction approach to enable the data to be analysed and more robust summary statistics to be calculated.

2. Methods

2.1. Database reconstruction

One option for deriving summary statistics is to use each summarised data line n_i times within the analysis, but this creates artificial discrete data clusters within a resulting distribution and does not account for the variation described within the summarised data. An alternative is to treat each summarised data line as $n_i = 1$, but this also 'loses' information on within study variation and omits the weighting of larger studies compared with smaller studies (this is the approach used in the IAEA data collation for human foodstuffs (IAEA, 2009; IAEA, 2010)). Therefore, a more statistically defensible approach, assuming data are lognormally distributed, is to use the summarised data from each individual study to generate a lognormal distribution and then randomly sample n_i times within that distribution to approximate the underlying dataset that produced the summarised data.

For each individual study for which summarised data are provided, the arithmetic mean ($\mu_{\ln x}$) of the natural logarithms of the underlying data values (x) and the corresponding standard deviation ($\sigma_{\ln x}$) are derived as:

$$\mu_{\ln x} = \ln \mu_x - \frac{1}{2}\sigma^2_{\ln x} \tag{12}$$

$$\sigma_{\ln x} = \sqrt{\ln\left(1 + \frac{\sigma_x^2}{\mu_x^2}\right)} \tag{13}$$

Assuming that the distribution of the untransformed data is lognormal, the natural logarithms of the dataset will follow a normal distribution. Therefore, the arithmetic mean of the natural logarithms of the underlying data values and the corresponding standard deviation describe a normal distribution. To sample n_i times within this distribution it is necessary to derive n_i random percentile values and determine the value of $\ln x$ at each percentile. These values can then be reverse transformed to the corresponding value of x in the original scale ($\exp^{\ln x} = x$). The random percentile values were derived using the MS Excel™ 2007 random number generator.

Given that the arithmetic mean of the natural logarithms of the underlying data values and the corresponding standard deviation describe a normal distribution, $\ln x$ can be standardised to derive the standard normal distribution random variable z, which defines the distance in standard deviation units between $\ln x$ and the arithmetic mean of the natural logarithms of variable x:

$$z = \frac{\ln x - \mu_{\ln x}}{\sigma_{\ln x}} \tag{14}$$

Published 'z tables' relate z values to specific probabilities of the standard normal distribution. For example, the probabilities for z values of -2 and $+2$ are 0.0228 and 0.9772 respectively, so approximately 95% of the values within the standard normal distribution occur within 2 standard deviation units of the arithmetic mean. For the purposes of the analysis presented here, we needed to derive values of $\ln x$ for specific percentiles, so Equation (14) was modified to:

$$z_p = \frac{\ln x_p - \mu_{\ln x}}{\sigma_{\ln x}} \tag{15}$$

where z_p is the value of z at probability p, x_p is the value of x at probability p and all other terms have been defined. The n_i randomly generated percentiles were converted to probabilities by dividing by 100 and the corresponding z values for each probability obtained from a 'z table', as reproduced in most statistics textbooks. Equation (15) was rearranged to calculate x_p:

$$x_p = \exp(\sigma_{\ln x} z_p + \mu_{\ln x}) \tag{16}$$

The calculated values of x_p for each study from which summarised data had been reported were used to replace the summarised data line for that study within the subsequent data analysis.

For studies reporting $n_i > 2$ and an arithmetic mean but not a standard deviation, we needed to estimate the arithmetic standard deviation. For a given wildlife group-radionuclide combination, the coefficient of variation (CV) was calculated for each study reporting both an arithmetic mean and a standard deviation:

$$\mathrm{CV} = \frac{\sigma_i}{\mu_i} \tag{17}$$

For each radionuclide, the arithmetic mean of the CVs (CV_μ) for the wildlife group was used to estimate the missing arithmetic standard deviation values (σ_i):

$$\sigma_i = \mathrm{CV}_\mu \cdot \mu_i \tag{18}$$

The calculation approach described above was implemented using a purpose-built spreadsheet (available at https://wiki.ceh.ac.uk/x/PgC6Cw). The resultant dataset (referred to hereafter as the reconstructed database or RDB) was used to derive full summary statistics: N, means, standard deviations, minimum, maximum and 95th percentile values. Equations (4), (5), (8) and (9) were used to calculate the arithmetic weighted mean and standard deviation and the geometric mean and standard deviation from the RBD. The min and max values were taken to be the minimum and maximum for each category within the RDB derived by applying Equation (16). Two estimates of 95th percentile were made: (i) from weighted arithmetic mean and standard deviation assuming a lognormal distribution and using Equation (16); and (ii) from weighted geometric mean and standard deviation using the following equation:

$$GM_{95} = \exp\left(\ln \mu_{gw} + 1.645 \cdot \ln \sigma_{gw}\right) \quad (19)$$

where GM_{95} is the 95th percentile estimated from the geometric summary statistics and 1.645 is the z value for the 95th percentile.

2.2. Statistical approach to sub-category comparison

The RDB was used to test for significant differences between sub-categories (wildlife sub-categories, habitats and stable element v's radioisotope) for examples with comparatively large N ($N > 40$). Minitab v16 was used to analyse the log-transformed data using a General Linear Model with Tukey's pairwise comparisons (see Minitab v16 help file).

3. Results and discussion

3.1. Improving WTD summary statistics

Table 3 compares the WTD summary statistics presented in IAEA (2013) with those calculated in the present paper using the data within the RDB; although not presented in IAEA (2013), for comparative purposes we have calculated 95th percentiles (as described above) from the IAEA summarised data.

There is little difference in the estimates of arithmetic mean, which demonstrates that both the IAEA WTD approach and the approach presented in this paper can be used. The arithmetic standard deviations are generally similar between the two approaches because the missing standard deviation values for data from particular sources were derived from the arithmetic mean of the coefficients of variation for the full dataset. Any differences in arithmetic standard deviation are not consistent, reflecting the random sampling taking place within the distributions for each individual data source and the location of data sources with missing values within the overall data distribution.

The geometric mean as presented by the IAEA is consistently higher than that calculated for the RDB, whilst the geometric standard deviation is consistently lower. IAEA (2013) acknowledges that the geometric mean and associated standard deviation values are approximations as Equations (10) and (11) are dependent upon the distribution of the underlying data. It is evident from the RDB arithmetic mean and standard deviation values presented in Table 3 that, if the approach outlined in IAEA (2013) was used to estimate geometric statistics, the same values as obtained by calculating geometric mean and standard deviation from the full dataset would not be estimated (e.g. Cs transfer to grasses and herbs and Pb transfer to arthropods, where the arithmetic statistics are similar for both IAEA and RDB, but the geometric statistics differ). Whilst IAEA could not assess the distribution of the underlying data, we have investigated the distributions present within each RDB for the various element-organism combinations considered and found that they all tend towards lognormal (e.g. Figs. 1 and 2). For the mammal Am $CR_{wo\text{-}media}$ dataset, the Kolmogorov–Smirnov test (K–S $Z = 1.251$, $p < 0.1$) indicates that the observed cumulative distribution function (OBD cdf) is not significantly different from the cdf that would be expected (EXP cdf) if the data are lognormal (Fig. 1). For the shrub Cs $CR_{wo\text{-}media}$ data, the Kolmogorov–Smirnov test (K–S $Z = 1.455$, $p < 0.05$) indicates that the OBD cdf are significantly different from the cdf that would be expected (EXP cdf) if the data are lognormal (Fig. 2). However, Fig. 2 suggests that the data are tending towards lognormal.

As expected, the calculated ranges for the RDB are consistently broader than those reported in the WTD. For the examples considered, the extent of the difference in range values is relative to the proportion of the WTD data which are summarised values, with greater variation between ranges being observed when the underlying dataset contains predominantly summarised data. For example, the data underlying the Am mammal data shown in Table 3 are all summarised data. The maximum value within the WTD of 0.17 is an arithmetic mean with an associated standard deviation of 0.36. It is therefore not surprising that the maximum value calculated within the RDB is considerably higher.

Some of the currently available assessment models utilise 95th percentile values in the screening level assessment tiers. In the ERICA Tool the 95th percentile is estimated from the arithmetic mean and standard deviation assuming a lognormal distribution. Given that the WTD geometric statistics are directly estimated from the arithmetic summary statistics, it is unsurprising that the two approaches to estimating the 95th percentile ($Lognorm_{95}$ and GM_{95}) give similar values. However, for the reconstructed database, the GM_{95} values are higher (by up to a factor of *circa* 2) than the $Lognorm_{95}$ values, with the exception of Pu mammal.

3.2. Testing the robustness of the RDB approach

The predictive capability of the RDB approach was assessed using three datasets for which all individual values were available: (i) ^{90}Sr activity concentrations in small mammals from the Chernobyl exclusion zone (additional data from the study described by Beresford et al., 2008d); (ii) ^{137}Cs activity concentrations in invertebrates from coastal sand dunes close to the Sellafield reprocessing plant (UK) (Wood et al., 2008, 2009a, 2009b); and (iii) ^{210}Pb activity concentrations in rabbits (RIFE, 1996, 1998, 1999, 2000, 2002, 2003, 2004). Table 4 compares summary statistics estimated directly from the individual data with those generated using the RDB approach having input arithmetic means and associated standard deviations estimated for sub-groups of the data (e.g. by species etc.). These sub-group arithmetic means and standard deviations were also used to generate overall summary statistics using the approach adopted within the WTD (Table 4). There was good agreement between the arithmetic mean and standard deviation values derived using all three approaches, with the WTD approach giving the closest agreement to the actual data. For geometric mean and standard deviation, the RDB approach provided a better estimate than the WTD approach. Whilst not predicting the absolute range observed in the source data the RDB approach gave better estimates than those derived from the summarised data (i.e. as per the WTD) alone.

Given that the RDB approach uses a probabilistic approach to generate a reconstructed dataset, there is a need to evaluate the potential variability in the result obtained. The Cs mammal data (not including *Rangifer* species, which is the approach used to summarise mammal data within the WTD) were used to generate a reconstructed dataset five times. The range in resultant arithmetic mean values was less than 15% with the arithmetic standard deviation value varying by 60%; geometric mean and standard deviation values were similar across all five simulations. The Cs mammal dataset was comparatively large ($N = 2463$) so repeat simulations were also undertaken for two relatively small subsets (Arctic fox ($N = 10$) and moose ($N = 3$)). Less than 20% variation was observed for any of the arithmetic and geometric summary parameters for the Arctic fox data. Whilst the mean values and the geometric standard deviation were generally similar (within 3%) across the simulations for the smaller moose datasets, the arithmetic standard deviation varied by an order of magnitude. We are aware that McCullough (2008) questioned the implementations of the Wichmann-Hill random number generator algorithm (Wichman and Hill, 1982) within Excel™ 2007. It is unclear whether

Table 3
Comparison of wildlife group $CR_{wo\text{-}media}$ summary statistics calculated using the IAEA WTD (Howard et al., 2013a) approach and the RDB approach presented in this paper.

Element	Wildlife group	Data source[a]	N (% of studies with $n_i > 2$, but no SD)	Arithmetic mean ± SD	Geometric mean (SD)	Lognorm95[b]	GM95[c]	Range
Am	Mammal[d]	IAEA	139	(3.2 ± 10)E-2	9.8E-3(4.7)	1.2E-1	1.2E-1	2.6E-4–1.7E-1
		RDB	139 (0%)	(4.6 ± 17)E-2	6.2E-3(10.4)	2.0E-1	2.9E-1	5.1E-6–1.7
Cs	Grasses & Herbs	IAEA	2028	1.2 ± 2.6	5.1E-1(3.7)	4.5	4.4	1.9E-3–37
		RDB[e]	2028 (20%)	1.2 ± 2.7	2.3E-1(9.0)	4.4	8.6	2.0E-5–41
Cs	Mammal[d]	IAEA	2463	3.5 ± 8.3	1.3(4.0)	13	13	2.8E-3–140
		RDB[e]	2463 (2%)	3.4 ± 7.8	1.2(5.2)	12	19	1.5E-3–140
Cs	Shrub	IAEA	354	2.3 ± 4.0	1.2(3.3)	8.2	8.0	9.8E-3–16
		RDB[e]	354 (7%)	2.3 ± 4.1	6.5E-1(5.4)	7.9	11	4.9E-3–30
Pb	Annelid	IAEA	647	(5.2 ± 7.5)E-1	2.9E-1(2.9)	1.7	1.7	2.3E-3–2.8
		RDB[e]	647 (50%)	(5.2 ± 7.5)E-1	1.2E-1(7.8)	1.7	3.5	1.1E-3–2.8
Pb	Arthropod	IAEA	561	(4.0 ± 4.7)E-1	2.6E-1(2.5)	1.2	1.2	4.6E-3–1.0
		RDB[e]	561 (64%)	(4.0 ± 4.6)E-1	9.6E-2(7.9)	1.2	2.9	4.6E-3–2.2
Pb	Mammal[d]	IAEA	515	(3.8 ± 3.6)E-2	2.8E-2(2.2)	1.0E-1	1.0E-1	2.7E-4–2.0E-1
		RDB[e]	515 (6%)	(3.8 ± 2.8)E-2	2.6E-2(3.2)	1.0E-1	1.7E-1	7.7E-6–3.3E-1
Pu	Arthropod	IAEA	150	(3.1 ± 4.9)E-2	1.7E-2(3.1)	1.1E-1	1.0E-1	4.2E-4–2.5E-1
		RDB	150 (0%)	(3.0 ± 4.5)E-2	9.7E-3(5.8)	1.0E-1	1.7E-1	2.1E-4–2.5E-1
Pu	Mammal[d]	IAEA	219	(5.0 ± 26)E-2	9.3E-3(6.3)	2.0E-1	1.9E-1	1.6E-4–2.6
		RDB[e]	219 (3%)	(5.4 ± 24)E-2	3.0E-3(8.5)	2.0E-1	1.0E-1	3.7E-5–2.6
Sr	Grasses & Herbs	IAEA	519	(9.8 ± 18)E-1	4.7E-1(3.4)	3.5	3.4	6.7E-3–8.8
		RDB[e]	519 (41%)	(9.8 ± 19)E-1	2.1E-1(6.6)	3.5	4.8	5.7E-4–15
Sr	Shrub	IAEA	307	(4.8 ± 7.8)E-1	2.5E-1(3.1)	1.7	1.6	4.7E-3–6.7
		RDB	307 (0%)	(4.9 ± 7.8)E-1	1.0E-1(9.0)	1.7	3.9	3.8E-4–6.7

[a] IAEA from handbook of radionuclide transfer parameters for wildlife (IAEA, 2013), RDB values estimated from the reconstructed database.
[b] The 95th percentile $CR_{wo\text{-}soil}$ value estimated from the arithmetic mean and standard deviation using Tier 3 of the ERICA Tool and assuming a log-normal distribution.
[c] The 95th percentile $CR_{wo\text{-}soil}$ value calculated from the geometric mean and standard deviation.
[d] Does not include *Rangifer* spp. (as per IAEA, 2013).
[e] Included data entries where $n_i > 2$ but no SD reported, which required SD values to be generated using the approach described in the text.

Microsoft has addressed the issues raised by McCullough, but the results of our repeat testing suggest that any issues concerning Excel's random number generation do not significantly affect our implementation of the methodology described above. If considerably larger datasets were being considered then we recommend that different random number generator options are tested (L'Ecuyer, 2012).

These evaluations give us some confidence in the outputs of the RDB approach.

3.3. Terrestrial wildlife group sub-category $CR_{wo\text{-}media}$ values

The $CR_{wo\text{-}media}$ data summarised by selected wildlife group sub-categories are presented in Table 5. The approach to database reconstruction has enabled us to test for significance between sub-categories for a selection of radionuclide-wildlife group combinations. In some instances, there are no significant differences between sub-categories (e.g. Cs and Sr transfer to broadleaf and coniferous trees and Cs transfer to arthropods), perhaps

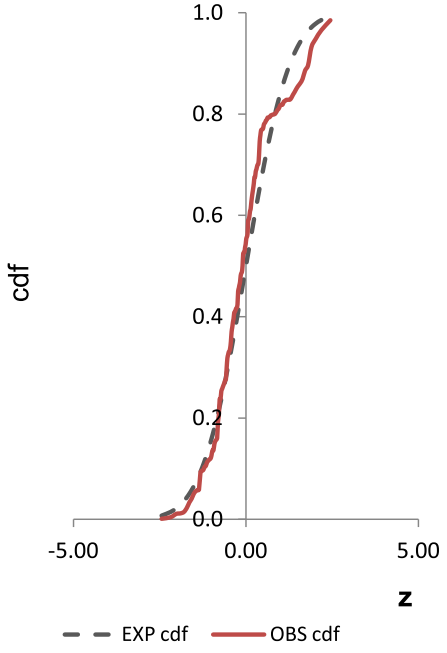

Fig. 1. Cumulative distribution function (cdf) for the natural logarithms of the mammal Am $CR_{wo\text{-}media}$ dataset ($N = 139$). OBS cdf = observed cdf; EXP cdf = expected cdf for a lognormal distribution.

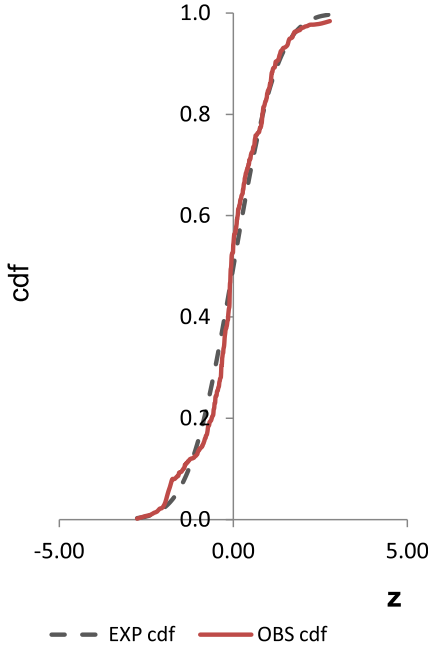

Fig. 2. Cumulative distribution function for the natural logarithms of the shrub Cs $CR_{wo\text{-}media}$ dataset ($N = 354$). OBS cdf = observed cdf; EXP cdf = expected cdf for a lognormal distribution.

Table 4
Comparison of summary statistics derived from source data or using the WTD and RDB approaches.

Element	Wildlife group	Approach	*N*	Arithmetic mean ± SD	Geometric mean (SD)	Range
Cs	Invertebrate	Source data	72	(2.4 ± 3.0)E-2	1.1E-2 (3.8)	2.6E-4–1.3E-1
		WTD	72	(2.4 ± 3.0)E-2	1.5E-2 (2.7)	1.4E-2–6.5E-2
		RDB	72	(2.5 ± 2.9)E-2	1.4E-2 (3.0)	1.2E-3–1.2E-1
Pb	Mammal (rabbit)	Source data	21	(2.3 ± 2.2)E-2	1.6E-2(2.5)	2.8E-3–9.0E-2
		WTD	21	(2.3 ± 2.2)E-2	1.7E-2(2.2)	5.9E-3–4.4E-2
		RDB	21	(2.3 ± 2.0)E-2	1.5E-2 (2.5)	3.4E-3–6.8E-2
Sr	Mammal	Source data	49	3.8 ± 3.4	2.6 (2.6)	1.9E-1–17
		WTD	49	3.8 ± 3.4	2.8 (2.2)	6.9E-1–5.4
		RDB	49	3.7 ± 3.0	2.7 (2.3)	3.5E-1–13

demonstrating that in such cases the generic wildlife group $CR_{wo\text{-}media}$ value is a suitable predictor of transfer. For all mammal comparisons, with the exception of Pu, *Rangifer* species had significantly higher transfer than other mammal groups. This appears to justify the approach taken by IAEA (2013) to exclude *Rangifer* data from the derivation of mammal $CR_{wo\text{-}media}$ values on the basis that this would skew the resultant summary statistics due to the unusual transfer pathway for this mammal sub-category (Howard et al., 1991).

Previous studies have suggested that the transfer of Cs to carnivorous vertebrates (such as canine and feline species) is higher than to vertebrates at lower trophic levels (Lowe and Horrill, 1991; Gaare and Staarland, 1994; Pendleton et al., 1964). However, the data for mammals in Table 5 show a significantly higher transfer to herbivorous and omnivorous species than to carnivorous species. Investigation of the WTD source literature revealed that over 50% of the mammals classified as carnivorous are actually insectivorous bat species and small mammals, such as species of mole and shrew,

Table 5
$CR_{wo\text{-}media}$ summary statistics for wildlife group sub-categories, calculated using the RDB approach.

Element	Wildlife group	Wildlife sub-category	*N*	Arithmetic mean ± SD	Geometric mean (SD)[a]	Reference ID[b] (n_i)
Am	Arthropod	Carnivorous	6	(7.2 ± 4.4)E-2	6.2E-2 (1.6)*	170(3), 488(3)
		Detritivorous	29	(1.2 ± 1.5)E-1	6.8E-2 (3.2)*	170(7), 172(4), 223(2), 488(16)
		Herbivorous	9	(1.9 ± 5.6)E-1	6.1E-3 (11.1)$^{\#}$	170(3), 407(6)
Am	Mammal	Carnivorous	13	(1.1 ± 2.9)E-1	5.8E-3 (11.6)$^{\#,+}$	197(9), 488(4)
		Herbivorous	27	(8.0 ± 32)E-2	1.2E-3 (29.4)$^{+}$	184(13), 407(8), 488(6)
		Omnivorous	84	(3.1 ± 5.4)E-2	1.2E-2 (5.2)$^{\#}$	221(28), 245(47), 488(9)
		Rangifer spp.[c]	9	(1.2 ± 0.6)E-1	1.0E-1 (1.76)*	197(9)
Cs	Arthropod	Carnivorous	15	(2.4 ± 4.7)E-1	4.1E-2 (6.7)*	170(6), 195(6), 488(3)
		Detritivorous[d]	56	(1.1 ± 2.7)E-1	3.1E-2 (4.1)*	169(8), 170(7), 172(4), 223(3), 257(18), 488(16)
		Herbivorous[d]	5	(3.7 ± 2.8)E-2	2.9E-2 (2.0)*	170(5)
Cs	Bird	Carnivorous	11	(1.5 ± 1.8)E-1	6.0E-2 (5.5)$^{\#}$	190(7), 405(4)
		Herbivorous	57	1.0 ± 1.5	3.2E-1 (4.8)*	163(5), 190(2), 228(40), 258(4), 263(1), 405(4), 486(1)
		Omnivorous	79	(6.1 ± 19)E-1	1.8E-1 (4.3)$^{*,\#}$	189(55), 190(9), 405(13), 486(2)
Cs	Mammal	Carnivorous	231	(5.4 ± 19)E-1	1.4E-1 (4.1)$^{}$	190(12), 275(5), 405(12), 06(119), 486(1), 488(8)
		Herbivorous	1879	3.8 ± 8.4	1.8 (3.5)$^{\#}$	163(202), 184(14), 190(73), 208(1), 209(1221), 228(26), 230(9), 242(25), 268(11), 288(12), 294(266), 405(15), 486(4)
		Omnivorous	333	3.3 ± 6.0	1.0 (6.2)$^{+}$	168(104), 190(75), 268(74), 289(25), 405(22), 486(15), 488(18)
		Rangifer spp.[c]	916	17 ± 16	11 (3.1)*	160(1), 163(414), 164(7), 218(2), 228(459), 241(33)
Cs	Tree	Broadleaf	252	(1.4 ± 2.0)E-1	6.3E-2 (4.1)*	190(21), 210(970), 265(9), 470(1), 471(3), 472(27), 473(11), 474(5), 475(7), 477(4), 478(3), 484(65), 485(1), 519(1)
		Coniferous	235	(1.4 ± 2.5)E-1	6.2E-2 (3.8)*	189(90), 472(33), 474(2), 475(5), 476(3), 484(102)
Pu	Arthropod	Carnivorous	9	(1.5 ± 0.9)E-2	1.2E-2 (2.3)*	170(3), 488(6)
		Detritivorous	68	(3.2 ± 4.7)E-2	8.2E-3 (7.1)*	170(7), 216(23), 223(6), 488(32)
		Herbivorous	8	(1.3 ± 0.9)E-3	9.9E-4 (2.1)$^{\#}$	261(2), 407(6)
Pu	Mammal	Carnivorous	29	(5.3 ± 6.1)E-3	2.1E-3 (5.0)*	197(9), 405(12), 488(8)
		Herbivorous	56	(6.0 ± 21)E-2	2.3E-3 (11.5)*	184(14), 222(1), 268(2), 405(15), 407(12), 488(12)
		Omnivorous	113	(5.8 ± 29)E-2	4.0E-3 (6.7)*	221(22), 245(47), 268(4), 405(22), 488(18)
		Rangifer spp.[c]	9	(4.2 ± 4.0)E-3	2.9E-3 (2.4)*	197(9)
Sr	Bird	Carnivorous	10	(1.9 ± 2.4)E-1	9.0E-2 (4.4)$^{\#}$	190(6), 405(4)
		Herbivorous	7	(3.1 ± 2.7)E-1	2.1E-1 (5.6)$^{*,\#}$	190(1), 263(1), 405(4), 486(1)
		Omnivorous	74	(5.1 ± 10)E-1	2.5E-1 (2.8)*	189(55), 190(6), 405(13)
Sr	Mammal	Carnivorous	164	(8.6 ± 15)E-1	3.5E-1 (3.8)$^{+}$	190(8), 405(12), 406(144)
		Herbivorous	108	2.6 ± 3.0	7.7E-1 (7.0)$^{\#}$	163(3), 190(53), 228(26), 268(11), 405(15)
		Omnivorous	202	1.8 ± 2.3	8.7E-1 (3.7)$^{\#}$	190(59), 245(47), 268(74), 405(22)
		Rangifer spp.[c]	435	6.5 ± 4.1	4.6 (2.8)*	160(1), 163(136), 218(2), 228(296)
Sr	Tree	Broadleaf	114	(4.4 ± 7.1)E-1	1.3E-1 (5.3)*	190(7), 473(11), 478(3), 480(3), 482(20), 484(45), 485(1)
		Coniferous	74	(5.6 ± 15)E-1	8.2E-2 (6.0)*	479(1), 480(1), 482(6), 484(66)

[a] Means with the same symbol are not significantly different ($p > 0.05$), significance was tested using general linear model with natural log data.
[b] For consistency with ICRP (2009), IAEA (2013) the reference ID numbers for the underlying database as described by Copplestone et al. (2013) are used (see Annex 1 for source reference information).
[c] *Rangifer* spp. data are not included in the herbivorous mammal data.
[d] IAEA (2013) has data from Crossley et al. (1973) [Reference ID 175] wrongly categorised by feeding type. These data have been removed and are not considered here.

Table 6
$CR_{wo\text{-}media}$ summary statistics for habitat sub-categories, calculated using the RDB approach.

Element	Wildlife group	Habitat sub-category	*N*	Arithmetic mean ± SD	Geometric mean (SD)[a]	Reference ID[b] (n_i)
Am	Arthropod	Forest	34	(2.0 ± 4.3)E-1	7.9E-2 (3.6)*	170(28), 172(4), 223(2)
		Coastal sand dunes	40	(6.5 ± 14)E-2	2.7E-2 (3.5)$^{\#}$	488(40)
		Semi-natural grassland	8	(4.0 ± 7.1)E-2	4.8E-3 (8.6)$^{+}$	382(2), 407(6)
Am	Mammal	Forest	62	(2.7 ± 2.2)E-2	1.4E-2 (4.0)*	172(15), 245(47)
		Coastal sand dunes	19	(3.9 ± 2.3)E-4	3.2E-4 (1.9)$^{\#}$	488(19)
		Semi-natural grassland	45	(1.0 ± 2.9)E-1	1.9E-2 (5.7)*	197(9), 221(28), 407(8)
Cs	Amphibian	Forest	7	(4.7 ± 1.9)E-1	4.4E-1 (1.5)*	188(7)
		Coastal sand dunes	39	(9.8 ± 8.1)E-2	7.5E-2 (2.1)$^{\#}$	486(39)
		Wetland	91	(4.9 ± 4.6)E-1	2.7E-1 (6.2)*	188(4), 205(82), 256(6)
Cs	Arthropod	Forest	64	(1.2 ± 2.6)E-1	4.0E-2 (4.0)*	170(39), 172(4), 223(3), 257(18)
		Coastal sand dunes	40	(2.5 ± 5.3)E-2	7.8E-3 (4.4)$^{\#}$	488(40)
		Semi-natural grassland	10	(2.4 ± 2.0)E-2	1.9E-2 (2.0)$^{*,\#}$	382(3), 388(7)
Pu	Arthropod	Forest	29	(4.0 ± 4.1)E-2	2.4E-2 (2.9)*	170(23), 223(6)
		Coastal sand dunes	80	(2.8 ± 3.7)E-2	1.6E-2 (3.1)$^{*,\#}$	488(80)
		Semi-natural grassland	10	(5.5 ± 7.5)E-2	6.2E-3 (13)$^{\#}$	382(4), 407(6)
Pu	Mammal	Forest	111	(5.7 ± 12)E-3	2.3E-3 (4.1)$^{\#}$	172(15), 245(47), 405(49)
		Coastal sand dunes	38	(7.9 ± 4.3)E-4	7.1E-4 (1.6)$^{+}$	488(38)
		Semi-natural grassland	21	(1.4 ± 3.2)E-1	1.4E-2 (17)*	197(9), 407(12)
Sr	Shrub	Forest	12	(4.2 ± 3.2)E-1	3.1E-1 (2.6)*	467(11), 468(1)
		Semi-natural grassland	60	(9.2 ± 5.8)E-2	7.7E-2 (1.8)$^{\#}$	164(60)
		Wetland	45	(5.5 ± 2.6)E-2	4.9E-2 (1.7)$^{+}$	164(45)

[a] Means with the same symbol are not significantly different ($p > 0.05$), significance was tested using general linear model with natural log data.
[b] For consistency with ICRP (2009) and IAEA (2013) the reference ID numbers for the underlying database as described by Copplestone et al. (2013) are used (see Annex 1 for source reference information).

rather that 'classical' carnivorous mammals such as canine species. For birds, the $CR_{wo\text{-}media}$ value for herbivorous species is significantly higher than that for carnivorous, again carnivorous bird data are dominated by insectivorous species (*Lanius collurio* and *Ficedula* sp.) and all carnivorous bird data originated from the Chernobyl exclusion zone. Most of the herbivorous bird data are for *Lagopus lagopus*, which inhabits areas with relatively high radiocaesium transfer.

3.4. Terrestrial habitat sub-category $CR_{wo\text{-}media}$ values

Table 6 summarises and compares CR data by habitat sub-category. In general, organisms in coastal sand dunes have lower $CR_{wo\text{-}media}$ values than other terrestrial sites as reported in previous studies (Wood et al., 2008, 2009a and 2009b). However, all the coastal sand dune data originate from two sites close to the Sellafield reprocessing plant where sea-to-land transfer of actinides and aerial deposition of other radionuclides are thought to be the main transport routes rather than root uptake (Wood et al., 2009a). Conversely, $CR_{wo\text{-}media}$ values for forest tend to be higher than those for the other habitats with which they can be compared (forest data originates from throughout Europe and one study in North America). It is necessary to evaluate sub-category values with caution; the habitat sub-category $CR_{wo\text{-}media}$ values have been calculated using the data for the broad wildlife group and may be influenced by the proportion of data coming from different wildlife sub-categories (and vice-versa).

3.5. Stable element versus radioisotope

Databases, such as the WTD, often amalgamate data by element, regardless of isotope (Copplestone et al., 2013). Increasing use of analytical techniques, such as ICP-MS, is producing total element data for application in radiological assessments (e.g. Barnett et al., 2013a; Beresford, 2010; Sheppard, 2013; Yankovich et al., 2013). Table 7 demonstrates significant differences between stable elements and radioisotopes for *Rangifer* species Pb $CR_{wo\text{-}media}$ values and shrub Sr $CR_{wo\text{-}media}$ values. Whilst we cannot explain the difference for Sr shrub data, we note that there is a bias in data sources. All of the stable Sr shrub $CR_{wo\text{-}media}$ data come from North America, predominantly Canada, whereas the majority of the ^{90}Sr data originate from Russia; *Vaccinium* spp. dominate both the stable Sr and ^{90}Sr entries. The difference in *Rangifer* species $CR_{wo\text{-}media}$ values for Pb is perhaps unexpected given that there is known to be a comparatively high transfer of ^{210}Pb via the aerial deposition − lichen − reindeer pathway (e.g. Thomas et al., 1994). Inspection of the lichen data within the WTD suggests that the $CR_{wo\text{-}media}$ for lichen is higher for ^{210}Pb than stable Pb.

4. Conclusions

Large variation between predicted and measured whole-body activity concentrations has been observed in various studies (e.g. Johansen et al., 2012; Wood et al., 2009b). This is highly likely to be due to the differences in site characteristics and the gross simplification in many models of representing transfer using one global

Table 7
Stable element and radioisotope $CR_{wo\text{-}media}$ value summary statistics, calculated using the RDB approach.

Element	Wildlife group	Isotope	*N*	Arithmetic mean ± SD	Geometric mean (SD)[a]	Reference ID[b] (n_i)
Pb	*Rangifer* spp.	Stable Pb	66	8.0 ± 3.9	6.5 (2.3)*	163(65), 218(1)
		^{210}Pb	204	2.2 ± 1.0	1.9 (1.7)$^{\#}$	214(24), 258(180)
Sr	Shrub	Stable Sr	131	1.1 ± 0.9	8.3E-1 (2.0)*	347(60), 348(60), 467(11)
		^{90}Sr	176	(5.1 ± 5.3)E-2	2.2E-2 (3.8)$^{\#}$	164(111), 252(64), 468(1)

[a] Means with the same letter are not significantly different ($p > 0.05$); significance tested using general linear model with natural log data.
[b] For consistency with ICRP (2009) and IAEA (2013) the reference ID numbers for the underlying database as described by Copplestone et al. (2013) are used (see Annex 1 for source reference information).

$CR_{wo\text{-}media}$ value for a given radionuclide-organism combination. A potential solution is to disaggregate summarised datasets, such as that presented in IAEA (2013), to estimate more refined $CR_{wo\text{-}media}$ values (e.g. for specific ecosystem types, wildlife groups etc.). The approach presented in this paper for analysing summarised datasets using a database reconstruction method has been demonstrated to be robust. It has enabled the statistical analysis of differences between ecosystem and wildlife group sub-categories and between stable elements and their radioisotopes.

$CR_{wo\text{-}media}$ value summary statistic derivation is confounded by the underlying dataset available to the IAEA. IAEA (2013) acknowledges that the methods used to estimate geometric statistics from the available data will result in approximations. Although we have shown that the WTD approach for calculating arithmetic summary statistics is fit-for-purpose, that for estimating geometric summary statistics is inadequate. We note that the ICRP have recommended geometric mean values for Reference Animals and Plants using the WTD approach (ICRP, 2009). We recommend that the approach derived in this paper be adopted to derive more robust geometric summary statistics.

Based on our evaluation of the current database, a number of the comparisons of $CR_{wo\text{-}media}$ values presented in Section 3 show statistically significant differences between habitat, wildlife group and isotope sub-categories (Tables 5–7). In some instances, the differences may be due to biases and limitations in the underlying database, casting doubt on the application of more refined $CR_{wo\text{-}media}$ values. Bayesian approaches, as discussed by Hosseini et al. (2013), may present an option for defining more refined $CR_{wo\text{-}media}$ values when few data are available.

The limited comparison between stable element and radioisotope data in Section 3.5 indicates significant differences for the two element-organism combinations considered, although these differences may be due to factors other than the isotope under consideration. An evaluation of stable Cs and ^{137}Cs $CR_{wo\text{-}media}$ values for freshwater fish from the WTD (Beresford et al., 2013) also showed significant differences, but again this may have been due to bias in the dataset. Rowan (2013) identified higher transfer of ^{137}Cs compared to stable Cs transfer to freshwater fish in a Canadian river, although the findings of Rowan are most probably explained by the pulsed releases of ^{137}Cs into the river. However, Barnett et al. (2013b) identified higher transfer of ^{137}Cs for forest plants and animals compared to stable Cs measured in the same samples. The differences observed by Barnett et al. (2013b) cannot be readily explained by data bias or site characteristics. There is clearly a need to undertake further research on the limitations of using stable element data for deriving radionuclide $CR_{wo\text{-}media}$ values, especially given the increase in the use of stable element data for this purpose, due to the cost-effectiveness of ICP-MS analysis (e.g. Barnett et al., 2013b; Beresford, 2010; Sheppard, 2013; Sheppard et al., 2010), and the dominance of stable element data within the WTD as demonstrated by Copplestone et al. (2013) for a selection of elements.

Environmental radiation protection models such as the ERICA Tool (Brown et al., 2008) adopt a tiered approach for assessing the impact of ionising radiation on wildlife. Tier 1 is a simple and highly conservative 'screening' assessment in which, if certain criteria are met, the assessor can exit the assessment process with a high level of confidence that there are no significant radiation impacts on biota and that no further action is required. Tier 2 provides a less conservative screening assessment in which the assessor can modify modelling parameters to produce a more realistic assessment. At Tier 3, the assessor can additionally undertake probabilistic assessment in an attempt to produce a realistic assessment of risk, with quantified uncertainty.

Uncertainty in modelling parameters leads to risk in decision making (Chen et al., 2011). Given the uncertainty in $CR_{wo\text{-}media}$ data, we suggest that summarised $CR_{wo\text{-}media}$ values are used with caution above the initial, highly conservative, screening-level assessments. This is consistent with the recommendation that site-specific data should be used for higher tier assessments (Brown et al., 2008; USDoE, 2002). However, generic $CR_{wo\text{-}media}$ values may have applicability in higher tier assessments for radionuclides contributing little to internal dose (Howard et al., 2013b). Alternative methods should be used to quantify transfer at higher assessment tiers if data are not available for the site (e.g. the phylogenetic approach proposed by Beresford et al. (2013), which accounts for the effect of site).

Acknowledgements

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Annex 1. Full source information for reference IDs used within the wildlife transfer database and quoted within Tables 5–7

Reference ID	Source
160	Bakunov, N.A., Panasenkova, O.I., Drichko, V.F., ^{90}Sr, ^{137}Cs and Natural Radionuclides in the Ecosystem of a Deep Lake., Russian J. Ecol. 30 (1998) 361–363. (in Russian).
163	Beresford, N.A. et al., Approaches to estimating the transfer of radionuclides to Arctic biota, Radioprotection 40 (2005) S285–S290.
164	Beresford, N.A., Wright, S.M., Brown, J.E., Sazykina, T., "Review of approaches for the estimation of radionuclide transfer to reference Arctic biota". (EPIC Deliverable 2) Centre for Ecology and Hydrology, Merlewood (2002).
168	Christaldi, M., Ieradi, L.A., Mascanzoni, D., Mattei, T., Environmental impact of the Chernobyl accident: mutagenesis in bank voles from Sweden, Int. J. Radiat. Biol. 59 (1991) 31-40.
169	Cooper, K., The effect of chronic radiation on invertebrate diversity and abundance within the chernobyl exclusion zone. Msc thesis (Restoration Ecology), University of Liverpool (2002)
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